

SEQUENCE LISTING

<110> MCGILL UNIVERSITY
GAGNON, Martin
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<120> LIGANDS OF GANGLIOSIDE GD2 AND USES THEREOF

<130> 82873-5

<140> NOT YET ASSIGNED
<141> 2003-09-19

<150> US 60/412,492
<151> 2002-09-20

<160> 23

<170> PatentIn version 3.2

<210> 1
<211> 13
<212> PRT
<213> Artificial

<220>
<223> GD2 Ligand

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa = Absent or Tyr or an analogue thereof.

<220>
<221> MOD_RES
<222> (1)..(1)
<223> The N-terminal group may be of the formula H2N-, RHN-, or, RRN-, wherein R at each occurrence is independently selected from (C1-C6) alkyl, (C1-C6) alkenyl, (C1-C6) alkynyl, substituted (C1-C6) alkyl, substituted (C1-C6) alkenyl, or substituted (C1-C6) alkynyl.

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> Xaa = Absent or Cys or an analogue thereof.

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa = Gly or Tyr or an analogue thereof.

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa = Gly or Cys or Tyr or an analogue thereof.

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa = Ile or Cys or an analogue thereof.

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<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa = Thr or Ala or an analogue thereof.

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa = Asn or an analogue thereof.

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> Xaa = Tyr or an analogue thereof.

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> Xaa = Asn or Gly or an analogue thereof.

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa = Ser or Cys or Val or Thr or an analogue thereof.

<220>
<221> MISC_FEATURE
<222> (11)..(11)
<223> Xaa = Ala or Cys or Tyr or His or Ser or an analogue thereof.

<220>
<221> MISC_FEATURE
<222> (12)..(12)
<223> Xaa = absent or Leu or Cys or Tyr or an analogue thereof.

<220>
<221> MISC_FEATURE
<222> (13)..(13)
<223> Xaa = absent or Met or Tyr or an analogue thereof.

<220>
<221> MOD_RES
<222> (13)..(13)
<223> C-terminal grp is of the formula -C(O)OH, -C(O)R, -C(O)OR,
-C(O)NHR, -C(O)NRR; wherein each R is independently selected from
(C1-C6) alkyl, (C1-C6) alkenyl, (C1-C6) alkynyl, substituted (C1-C6)
alkyl, substituted (C1-C6) alkenyl, or substituted (C1-C6) alkynyl.

<400> 1
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

<210> 2
<211> 13
<212> PRT
<213> Artificial

<220>
<223> GD2 Ligand

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<220>
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<223> Xaa = Absent or Tyr or an analogue thereof.

<220>
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<222> (2)..(2)
<223> Xaa = Absent or Cys or an analogue thereof.

<220>
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<222> (3)..(3)
<223> Xaa = Gly or Tyr or an analogue thereof.

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<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa = Gly or Cys or Tyr or an analogue thereof.

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<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa = Ile or Cys or an analogue thereof.

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<222> (6)..(6)
<223> Xaa = Thr or Ala or an analogue thereof.

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<221> MISC_FEATURE
<222> (7)..(7)
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<221> MISC_FEATURE
<222> (8)..(8)
<223> Xaa = Tyr or an analogue thereof.

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<221> MISC_FEATURE
<222> (9)..(9)
<223> Xaa = Asn or Gly or an analogue thereof.

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<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa = Ser or Cys or Val or Thr or an analogue thereof.

<220>
<221> MISC_FEATURE
<222> (11)..(11)
<223> Xaa = Ala or Cys or Tyr or His or Ser or an analogue thereof.

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<221> MISC_FEATURE
<222> (12)..(12)
<223> Xaa = Absent or Leu or Cys or Tyr or an analogue thereof.

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<222> (13)..(13)
<223> Xaa = Absent or Met or Tyr or an analogue thereof.

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<210> 3
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<220>
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Tyr Cys Thr Asn Tyr Gly Val Cys Tyr
1 5

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Gly Gly Ile Ala Asn Tyr Asn Thr Ser
1 5

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<400> 10
Tyr Cys Gly Gly Ile Ala Asn Tyr Asn Cys Tyr
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Tyr Cys Ile Ala Asn Tyr Asn Thr Cys Tyr
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<220>
<223> Spanning sequence for peptide analogs that actively inhibit
GD2-mAb 3F8 interactions.

<400> 13
Ile Thr Asn Tyr Asn
1 5

<210> 14
<211> 5
<212> PRT
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<220>
<223> Spanning sequence for peptide analogs that actively inhibit
GD2-mAb 3F8 interactions.

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1 5

<210> 15
<211> 11
<212> PRT
<213> Artificial

<220>
<223> Peptide Mimic

<220>
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<222> (1)..(11)
<223> Peptide is cyclic.

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<210> 16
<211> 8
<212> PRT
<213> Artificial

<220>
<223> Peptide Mimic

<220>
<221> MISC_FEATURE
<222> (1)..(8)
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1 5

<210> 17
<211> 9
<212> PRT
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<220>
<223> Peptide Mimic

<220>
<221> MISC_FEATURE
<222> (1)..(9)
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<210> 18
<211> 8
<212> PRT
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<220>
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<400> 18
Cys Thr Asn Tyr Gly Val His Cys
1 5

<210> 19
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<220>
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<220>
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<210> 20
<211> 9
<212> PRT
<213> Artificial

<220>
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<220>
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<222> (1)..(9)
<223> Peptide is cyclic.

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1 5

<210> 21
<211> 11
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<213> Artificial

<220>
<223> Peptide Mimic

<400> 21
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<210> 22
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<212> PRT
<213> Artificial

<220>
<223> Peptide mimic.

<220>
<221> MISC_FEATURE
<222> (1)..(8)
<223> Peptide is cyclic.

<400> 22

Cys Ile Ala Asn Tyr Asn Thr Cys

1

5

<210> 23

<211> 1358

<212> PRT

<213> Homo sapiens

<400> 23

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20 25 30Leu Glu Val Thr Thr Glu Arg Val Gln Arg Gln Ser Val Glu Glu Glu
35 40 45Gly Gly Ile Ala Asn Tyr Asn Thr Ser Ser Lys Glu Gln Pro Val Val
50 55 60Phe Asn His Val Tyr Asn Ile Asn Val Pro Leu Asp Asn Leu Cys Ser
65 70 75 80Ser Gly Leu Glu Ala Ser Ala Glu Gln Glu Val Ser Ala Glu Asp Glu
85 90 95Thr Leu Ala Glu Tyr Met Gly Gln Thr Ser Asp His Glu Ser Gln Val
100 105 110Thr Phe Thr His Arg Ile Asn Phe Pro Lys Lys Ala Cys Pro Cys Ala
115 120 125Ser Ser Ala Gln Val Leu Gln Glu Leu Leu Ser Arg Ile Glu Met Leu
130 135 140Glu Arg Glu Val Ser Val Leu Arg Asp Gln Cys Asn Ala Asn Cys Cys
145 150 155 160Gln Glu Ser Ala Ala Thr Gly Gln Leu Asp Tyr Ile Pro His Cys Ser
165 170 175Gly His Gly Asn Phe Ser Phe Glu Ser Cys Gly Cys Ile Cys Asn Glu
180 185 190Gly Trp Phe Gly Lys Asn Cys Ser Glu Pro Tyr Cys Pro Leu Gly Cys
195 200 205Ser Ser Arg Gly Val Cys Val Asp Gly Gln Cys Ile Cys Asp Ser Glu
210 215 220Tyr Ser Gly Asp Asp Cys Ser Glu Leu Arg Cys Pro Thr Asp Cys Ser
225 230 235 240Ser Arg Gly Leu Cys Val Asp Gly Glu Cys Val Cys Glu Glu Pro Tyr
245 250 255

Thr Gly Glu Asp Cys Arg Glu Leu Arg Cys Pro Gly Asp Cys Ser Gly
 260 265 270
 Lys Gly Arg Cys Ala Asn Gly Thr Cys Leu Cys Glu Glu Gly Tyr Val
 275 280 285
 Gly Glu Asp Cys Gly Gln Arg Gln Cys Leu Asn Ala Cys Ser Gly Arg
 290 295 300
 Gly Gln Cys Glu Glu Gly Leu Cys Val Cys Glu Glu Gly Tyr Gln Gly
 305 310 315 320
 Pro Asp Cys Ser Ala Val Ala Pro Pro Glu Asp Leu Arg Val Ala Gly
 325 330 335
 Ile Ser Asp Arg Ser Ile Glu Leu Glu Trp Asp Gly Pro Met Ala Val
 340 345 350
 Thr Glu Tyr Val Ile Ser Tyr Gln Pro Thr Ala Leu Gly Gly Leu Gln
 355 360 365
 Leu Gln Gln Arg Val Pro Gly Asp Trp Ser Gly Val Thr Ile Thr Glu
 370 375 380
 Leu Glu Pro Gly Leu Thr Tyr Asn Ile Ser Val Tyr Ala Val Ile Ser
 385 390 395 400
 Asn Ile Leu Ser Leu Pro Ile Thr Ala Lys Val Ala Thr His Leu Ser
 405 410 415
 Thr Pro Gln Gly Leu Gln Phe Lys Thr Ile Thr Glu Thr Thr Val Glu
 420 425 430
 Val Gln Trp Glu Pro Phe Ser Phe Ser Phe Asp Gly Trp Glu Ile Ser
 435 440 445
 Phe Ile Pro Lys Asn Asn Glu Gly Gly Val Ile Ala Gln Val Pro Ser
 450 455 460
 Asp Val Thr Ser Phe Asn Gln Thr Gly Leu Lys Pro Gly Glu Glu Tyr
 465 470 475 480
 Ile Val Asn Val Val Ala Leu Lys Glu Gln Ala Arg Ser Pro Pro Thr
 485 490 495
 Ser Ala Ser Val Ser Thr Val Ile Asp Gly Pro Thr Gln Ile Leu Val
 500 505 510
 Arg Asp Val Ser Asp Thr Val Ala Phe Val Glu Trp Ile Pro Pro Arg
 515 520 525
 Ala Lys Val Asp Phe Ile Leu Leu Lys Tyr Gly Leu Val Gly Gly Glu
 530 535 540
 Gly Gly Arg Thr Thr Phe Arg Leu Gln Pro Pro Leu Ser Gln Tyr Ser
 545 550 555 560
 Val Gln Ala Leu Arg Pro Gly Ser Arg Tyr Glu Val Ser Val Ser Ala
 565 570 575

Val Arg Gly Thr Asn Glu Ser Asp Ser Ala Thr Thr Gln Phe Thr Thr
 580 585 590
 Glu Ile Asp Ala Pro Lys Asn Leu Arg Val Gly Ser Arg Thr Ala Thr
 595 600 605
 Ser Leu Asp Leu Glu Trp Asp Asn Ser Glu Ala Glu Val Gln Glu Tyr
 610 615 620
 Lys Val Val Tyr Ser Thr Leu Ala Gly Glu Gln Tyr His Glu Val Leu
 625 630 635 640
 Val Pro Arg Gly Ile Gly Pro Thr Thr Arg Ala Thr Leu Thr Asp Leu
 645 650 655
 Val Pro Gly Thr Glu Tyr Gly Val Gly Ile Ser Ala Val Met Asn Ser
 660 665 670
 Gln Gln Ser Val Pro Ala Thr Met Asn Ala Arg Thr Glu Leu Asp Ser
 675 680 685
 Pro Arg Asp Leu Met Val Thr Ala Ser Ser Glu Thr Ser Ile Ser Leu
 690 695 700
 Ile Trp Thr Lys Ala Ser Gly Pro Ile Asp His Tyr Arg Ile Thr Phe
 705 710 715 720
 Thr Pro Ser Ser Gly Ile Ala Ser Glu Val Thr Val Pro Lys Asp Arg
 725 730 735
 Thr Ser Tyr Thr Leu Thr Asp Leu Glu Pro Gly Ala Glu Tyr Ile Ile
 740 745 750
 Ser Val Thr Ala Glu Arg Gly Arg Gln Gln Ser Leu Glu Ser Thr Val
 755 760 765
 Asp Ala Phe Thr Gly Phe Arg Pro Ile Ser His Leu His Phe Ser His
 770 775 780
 Val Thr Ser Ser Ser Val Asn Ile Thr Trp Ser Asp Pro Ser Pro Pro
 785 790 795 800
 Ala Asp Arg Leu Ile Leu Asn Tyr Ser Pro Arg Asp Glu Glu Glu Glu
 805 810 815
 Met Met Glu Val Ser Leu Asp Ala Thr Lys Arg His Ala Val Leu Met
 820 825 830
 Gly Leu Gln Pro Ala Thr Glu Tyr Ile Val Asn Leu Val Ala Val His
 835 840 845
 Gly Thr Val Thr Ser Glu Pro Ile Val Gly Ser Ile Thr Thr Gly Ile
 850 855 860
 Asp Pro Pro Lys Asp Ile Thr Ile Ser Asn Val Thr Lys Asp Ser Val
 865 870 875 880
 Met Val Ser Trp Ser Pro Pro Val Ala Ser Phe Asp Tyr Tyr Arg Val
 885 890 895

Ser Tyr Arg Pro Thr Gln Val Gly Arg Leu Asp Ser Ser Val Val Pro
 900 905 910
 Asn Thr Val Thr Glu Phe Thr Ile Thr Arg Leu Asn Pro Ala Thr Glu
 915 920 925
 Tyr Glu Ile Ser Leu Asn Ser Val Arg Gly Arg Glu Glu Ser Glu Arg
 930 935 940
 Ile Cys Thr Leu Val His Thr Ala Met Asp Asn Pro Val Asp Leu Ile
 945 950 955 960
 Ala Thr Asn Ile Thr Pro Thr Glu Ala Leu Leu Gln Trp Lys Ala Pro
 965 970 975
 Val Gly Glu Val Glu Asn Tyr Val Ile Val Leu Thr His Phe Ala Val
 980 985 990
 Ala Gly Glu Thr Ile Leu Val Asp Gly Val Ser Glu Glu Phe Arg Leu
 995 1000 1005
 Val Asp Leu Leu Pro Ser Thr His Tyr Thr Ala Thr Met Tyr Ala
 1010 1015 1020
 Thr Asn Gly Pro Leu Thr Ser Gly Thr Ile Ser Thr Asn Phe Ser
 1025 1030 1035
 Thr Leu Leu Asp Pro Pro Ala Asn Leu Thr Ala Ser Glu Val Thr
 1040 1045 1050
 Arg Gln Ser Ala Leu Ile Ser Trp Gln Pro Pro Arg Ala Glu Ile
 1055 1060 1065
 Glu Asn Tyr Val Leu Thr Tyr Lys Ser Thr Asp Gly Ser Arg Lys
 1070 1075 1080
 Glu Leu Ile Val Asp Ala Glu Asp Thr Trp Ile Arg Leu Glu Gly
 1085 1090 1095
 Leu Leu Glu Asn Thr Asp Tyr Thr Val Leu Leu Gln Ala Ala Gln
 1100 1105 1110
 Asp Thr Thr Trp Ser Ser Ile Thr Ser Thr Ala Phe Thr Thr Gly
 1115 1120 1125
 Gly Arg Val Phe Pro His Pro Gln Asp Cys Ala Gln His Leu Met
 1130 1135 1140
 Asn Gly Asp Thr Leu Ser Gly Val Tyr Pro Ile Phe Leu Asn Gly
 1145 1150 1155
 Glu Leu Ser Gln Lys Leu Gln Val Tyr Cys Asp Met Thr Thr Asp
 1160 1165 1170
 Gly Gly Gly Trp Ile Val Phe Gln Arg Arg Gln Asn Gly Gln Thr
 1175 1180 1185
 Asp Phe Phe Arg Lys Trp Ala Asp Tyr Arg Val Gly Phe Gly Asn
 1190 1195 1200

Val	Glu	Asp	Glu	Phe	Trp	Leu	Gly	Leu	Asp	Asn	Ile	His	Arg	Ile
1205						1210					1215			
Thr	Ser	Gln	Gly	Arg	Tyr	Glu	Leu	Arg	Val	Asp	Met	Arg	Asp	Gly
1220						1225					1230			
Gln	Glu	Ala	Ala	Phe	Ala	Ser	Tyr	Asp	Arg	Phe	Ser	Val	Glu	Asp
1235						1240					1245			
Ser	Arg	Asn	Leu	Tyr	Lys	Leu	Arg	Ile	Gly	Ser	Tyr	Asn	Gly	Thr
1250						1255					1260			
Ala	Gly	Asp	Ser	Leu	Ser	Tyr	His	Gln	Gly	Arg	Pro	Phe	Ser	Thr
1265						1270					1275			
Glu	Asp	Arg	Asp	Asn	Asp	Val	Ala	Val	Thr	Asn	Cys	Ala	Met	Ser
1280						1285					1290			
Tyr	Lys	Gly	Ala	Trp	Trp	Tyr	Lys	Asn	Cys	His	Arg	Thr	Asn	Leu
1295						1300					1305			
Asn	Gly	Lys	Tyr	Gly	Glu	Ser	Arg	His	Ser	Gln	Gly	Ile	Asn	Trp
1310						1315					1320			
Tyr	His	Trp	Lys	Gly	His	Glu	Phe	Ser	Ile	Pro	Phe	Val	Glu	Met
1325						1330					1335			
Lys	Met	Arg	Pro	Tyr	Asn	His	Arg	Leu	Met	Ala	Gly	Arg	Lys	Arg
1340						1345					1350			
Gln	Ser	Leu	Gln	Phe										
1355														